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FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCC
CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC
TTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG
CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG
ATTTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAAC
ACCATTGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG
TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC
CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT
CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTC
ATCGTCATTCCACTGATTGTTCATGATTGCCTGCTACTCCGTGGTGGTCTGTGCAGCCCGG
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCAGGATGAGAGT
GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG
GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCC
AGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT
AAGGAAGGCAGCACCAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTTCGCACAGAG
GTCAACCAGTGACGATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC
AATTTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCACCCAGTCGT
CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAAGTGCAAAGCTGCTAAAGTG
ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTC
CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC
TGGCTTTTCTTCTGCAAGTGTGATCCACCCCTATGTCTATGGCTACATGCACAAGACC
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA
GAAGATAGCCACCCAGACCTGCCCCGGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT
TCCTACGATTCTGCTACTTTTCTCTGA

FIG. 2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
QLLQVTNRFI FNLLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN
TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGSLLKAKEGSTGTSESSVEA
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYQCKAAKVI FIIIFSIVLSLGPYCFLAV
LAVWVDVETQVPQWVITII IWLFFLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK
EDSHPDLPGTEGGTEGKIVPSYDSATFP

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FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1	MTSTCTNSTR	ESNSSHTCMP	LSKMPISLAH	GIIRST	<u>VLVI</u>	<u>FLAASFVGNI</u>
51	<u>VLALVL</u> QRKP	QLLQVTNRFI	<u>FNLLVTDLLQ</u>	<u>ISLVAPWVVA</u>	<u>TSVPLEFWPLN</u>	
101	<u>SHFCTALVSL</u>	<u>THLFAFASVN</u>	<u>TIVLVSVD</u> RY	LSIIHPLSYP	SKMTQRR	<u>GYL</u>
151	<u>LLYGTWIVAI</u>	<u>LQSTPPLYGW</u>	GQAAFDERNA	LCSMIWGASP	SYT	<u>ILSVVSF</u>
201	<u>IVIPLIVMIA</u>	<u>CYSVVFCAAR</u>	RQHALLYNVK	RHSLEVRVKD	CVENEDEEGA	
251	EKKEEFQDES	EFRRQHEGEV	KAKEGRMEAK	DGSLKAKEGS	TGTSESSVEA	
301	RGSEEVRESS	TVASDGSMEG	KEGSTKVEEN	SMKADKGRTE	VNQC SIDLGE	
351	DDMEFGEDDI	NFSEDDVEAV	NIPESLPPSR	RNSNSNPPLP	RCYQCKAAK	<u>V</u>
401	<u>IFIIIFS</u> YVL	<u>SLGPYCFLAV</u>	LAVWVDVETQ	VPQ	<u>WVITIII</u>	<u>WLFFLQCCIH</u>
451	<u>PYVYG</u> YMHKT	IKKEIQDMLK	KFFCKEKPPK	EDSHPDLP	EGGT	EGKIVP
501	SYDSATFP					

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FIG. 6A

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~MANFTFGDLALDVARMGGLASTPSGLRSTGLTTPGLSPT
A1AD_HUMAN	MTRDILLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
A1AD_MOUSE	MTRDILSVTFEGPRASSSTGGSGAGGGAGTVG...P.EG
Q13675	~~~~~
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	~~~~~
O54913	~~~~~
A1AA_BOVIN	~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	~~~~~
A1AA_HUMAN	~~~~~
A1AA_ORYLA	~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~MHNLSAQPWQAKMANITYDNVTLSN
YDBM_CAEEL	MCFAEKGEAGEDVDHHSLEFC.P.KKLVGN...KGFIRN
5H1A_HUMAN	~~~~~MDV..LSPGQ...GNNTT...SPPAPFETGGN
5H1A_MOUSE	~~~~~MDM..FSLGQ...GNNTT...TSLEPFGTGGN
5H1A_FUGRU	~~~~~MDLRATSSND...SNATSGYSDTAAVDWDEGEN
5HT_LYMST	GLVTSDFNDSYGLT.GQFINGSHSSRSRDNASANDTSATN
A1AD_HUMAN	PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
A1AD_MOUSE	PAVGGVP.GATGGSVVGTGSGEDNQSSAEAGAA.ASGE
Q13675	~~~~~MVFLSGNASDS
Q13729	~~~~~MVFLSGNASDS
O60451	~~~~~MVFLSGNASDS
A1AA_RAT	~~~~~MVLLSENASEG
O54913	~~~~~MVLLSENASEG
A1AA_BOVIN	~~~~~MVFLSGNASDS
A1AA_CANFA	~~~~~MVFLSGNASDS
A1AA_RABIT	~~~~~MVFLSGNASDS
A1AA_HUMAN	~~~~~MVFLSGNASDS
A1AA_ORYLA	~~~~~MTPSSVTLNC
O96716	~~~~~MSANTTVSPTETTANTANSTEA
O75963	~~~~~MSLNSSLS
HGPRBMY8	~~~~~MTSTCTNSTRESNS

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FIG. 6B

ACM4_CHICK	RSEVAIQPPTNYKTVELVFIATVTGSLS..LVTVVGNILV
YDBM_CAEEL	QYH.....QHETIQ..ILKGSALFLLV..LWTIFANSLV
5H1A_HUMAN	ITG...ISDVTVSYQ..VITSLLLGTLLI..FCAVLGNACV
5H1A_MOUSE	DTG...LSNVTFYSYQ..VITSLLLGTLLI..FCAVLGNACV
5H1A_FUGRU	ATGSGSLPDEEISYQ..IITSIFLGALI..LCSTIFGNSCV
5HT_LYMST	MTDDRYWSLTVYSHEHLVLTSVILGLFV..LCCIIIGNCFV
A1AD_HUMAN	V.NGTAAVGGGLVVSAGGVGVFLAAFI..LMAVAGNLLV
A1AD_MOUSE	V.NGSAAVGGGLVVSAGGVGVFLAAFI..LTAVAGNLLV
Q13675	S.NCTQPPAP.VNISKAILLGVILGGLI..LFGVLGNILV
Q13729	S.NCTQPPAP.VNISKAILLGVILGGLI..LFGVLGNILV
O60451	S.NCTQPPAP.VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_RAT	S.NCTHPPAP.VNISKAILLGVILGGLI..IFGVLGNILV
O54913	S.NCTHPPAQ.VNISKAILLGVILGGLI..IFGVLGNILV
A1AA_BOVIN	S.NCTHPPPP.VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_CANFA	S.NCTHPPAP.VNISKAILLGVILGGLI..IFGVLGNILV
A1AA_RABIT	S.NCTHPPAP.VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_HUMAN	S.NCTQPPAP.VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_ORYLA	S.NCSHVLAPELNTVKAVVLGMVLGIFI..LFGVIGNILV
O96716	SVGSCFAPNPYSAGVOAV..LGLITVILI..LLTVIGNVLV
O75963	CRKELSNLTEEGEGGGVITQFIATIVITIEFVCLGNLVI
HGPRBMY8	SHTCMPLSKMPTSLAHGITRSTVL..VIFLAASFVGNIVL
ACM4_CHICK	MLSIKVNROLOTVNNYELFSLACADLIIGVFSMNLYTVYI
YDBM_CAEEL	FLVLYKNPRLQTVPNLLVGNLAFSDLALGLIVLPLSSVYA
5H1A_HUMAN	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_MOUSE	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_FUGRU	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5HT_LYMST	IAAVMLERSLHNVANLYLISLAVADLMVAVLVMPLSVVSE
A1AD_HUMAN	ILSVACNRHLOTVTNFYFIVNLAVADLLLSATVLPFSATME
A1AD_MOUSE	ILSVACNRHLOTVTNFYFIVNLAVADLLLSAAVLPFSATME
Q13675	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
Q13729	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
O60451	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_RAT	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
O54913	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_BOVIN	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_CANFA	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_RABIT	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_HUMAN	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_ORYLA	ILSVVCHRHLQTVTYFYFIVNLAVADLLLSSTVLPFSAIFE
O96716	ILAVTCHRKMRVTNFFIVSLACADLSVGITVLPFAATND
O75963	VVTLYKKSYYLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSS
HGPRBMY8	ALVLQRPQLLOVTNREFIENLLVTDLLQISLVAPWVVATS

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FIG. 6C

ACM4_CHICK	IKGYWPLGAVVCDLWLALDYVVSNASVMNLLTISFD	RYFC
YDBM_CAEEL	IAGEWVEPDALCEVFVSADILCSTASIWNLSIVGL	DRYWA
5H1A_HUMAN	VLNKWTLGQVTCDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5H1A_MOUSE	VLNKWTLGQVTCDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5H1A_FUGRU	VLNKWTLGQDICDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5HT_LYMST	ISKVWFLHSEVCDMWISVDVLCCTASILHLVAIAM	DRYWA
A1AD_HUMAN	VLGEWAFGRAFCDVWAAVDVLCCTASILSLCTISV	DRYVG
A1AD_MOUSE	VLGEWPFGRTFCDVWAAVDVLCCTASILSLCTISV	DRYVG
Q13675	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
Q13729	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
O60451	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RAT	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
O54913	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_BOVIN	ILGYWAFGRVFCNVWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_CANFA	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RABIT	ILGYWAFGRVFCNIWAAVDVLCCTASISLCVIS	DRYIG
A1AA_HUMAN	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_ORYLA	ILDRWVFGRVFCNIWAAVDVLCCTASIMSLCVIS	DRYIG
O96716	ILGYWPFGG.YCDVWVSFDVLNSTASILNLVVI	AFDRELA
O75963	IRREWIFGVVWCNFSALLYLLISSASMTLGVIA	TDRYYA
HGPRBMY8	VPLFWPLNSHECTALVSLTHLFAFASVNTIVLV	SVDRYLS
ACM4_CHICK	VTKPLTYPARRTTKMAGLMTAAAWTISFILWAPAT	.LFW.
YDBM_CAEEL	ITSPVAYMSKRNKRTAGIMTISVWISSATISLAPL	.LGWK
5H1A_HUMAN	ITDPIDYVNKRTPRRAAALISLTWLTIGFLISIPP	.LGW.
5H1A_MOUSE	ITDPIDYVNKRTPRRAAALISLTWLTIGFLISIPP	.LGW.
5H1A_FUGRU	ITDPIDYVNKRTPRRAAVLISVTWLTIGFSISIPP	.LGW.
5HT_LYMST	VTS.IDYIRRRSARRILMTMVVWIVALFISIPPL	.FGW.
A1AD_HUMAN	VRHSLKYPAIMTERKAAAILALTWVVALVSVSGPL	.LGW.
A1AD_MOUSE	VRHSLKYPAIMTERKAAAILALTWVVALVSVSGPL	.LGW.
Q13675	VSYPRLRYPTIMTQRRGLMALLCVWALSLVISIGPL	.FGW.
Q13729	VSYPRLRYPTIMTQRRGLMALLCVWALSLVISIGPL	.FGW.
O60451	VSYPRLRYPTIMTQRRGLMALLCVWALSLVISIGPL	.FGW.
A1AA_RAT	VSYPRLRYPTIMTQRRGVRALLCVWVLSLVISIGPL	.FGW.
O54913	VSYPRLRYPTIMTQRRGVRALLCVWALSLVISIGPL	.FGW.
A1AA_BOVIN	VSYPRLRYPTIMTQKRGMLALLCVWALSLVISIGPL	.FGW.
A1AA_CANFA	VSYPRLRYPTIMTQKRGMLALLCVWALSLVISIGPL	.FGW.
A1AA_RABIT	VSYPRLRYPTIMTQRRGLRALLCVWAFSLVISIGPL	.FGW.
A1AA_HUMAN	VSYPRLRYPTIMTQRRGLMALLCVWALSLVISIGPL	.FGW.
A1AA_ORYLA	VSYPRLRYPAIMTKRRALLAVMLLWVLSVISIGPL	.FGW.
O96716	ITAPFTYHTRMTERTAGILLATVWGTSLVVSFLP	IQAGWY
O75963	VLYPMVYPMKTTGNRAVMALVYIWLHSLIGCLPPL	.FGWS
HGPRBMY8	TIHPLSYPSKMTQRRGYLLLYGTWLVALLQSTPPL	.YGWG

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FIG. 6D

ACM4_CHICK	QFIVGKRTVHE.....RECYIQFLSNPAVTFGTAIAAFYL
YDBM_CAEEL	QTAQTENLIYEKNNTVRQC..TFLDLPSYTVYSATGSFFI
5H1A_HUMAN	R.TP.EDRSDPDA.....CTIS..KDHGYTIYSTFGAFYI
5H1A_MOUSE	R.AP.EDRSNPNE.....CTIS..KDHGYTIYSTFGAFYI
5H1A_FUGRU	R.SA.EDRANPDA.....CIIS..QDPGYTIYSTFGAFYI
5HT_LYMST	R.DPNNDPDKTGT.....CIIS..ODKGYTIYSTFGAFYL
A1AD_HUMAN	K.EPVPP.....DERFCGIT..EEAGYAVFSSVCSFYI
A1AD_MOUSE	K.EPVPP.....DERFCGIT..EEVGYATFSSVCSFYI
Q13675	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYL
Q13729	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYL
O60451	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYL
A1AA_RAT	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
O54913	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_BOVIN	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_CANFA	R.QPAPE.....DETICQIT..EPPGYVLFSAIGSFYV
A1AA_RABIT	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_HUMAN	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYL
A1AA_ORYLA	K.EPAPE.....DETICKIT..EPPGYATFSAIGSFYL
O96716	R.DNQSEALAIYSDPCLCIFT..ASTAYTIVSSILISFYI
O75963	S.VEFDEFKWM.....CVAAWH..REPGYTAFWQIWCALF
HGPRBMY8	QA.....AFDERNALCSMIWGASPSYTIILSVVSFIVI
ACM4_CHICK	PVIMTVLYIHTSTA.SRSRVRRHKPEsrkerkgksLSFF
YDBM_CAEEL	PTLLMFFVYFKIYQAFAKHRAQIYRQKVIRKHIESTILH
5H1A_HUMAN	PLLLMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_MOUSE	PLLLMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_FUGRU	PLLLMLVLYGRIFKA.....ARFRIRKTVKKTEKA.....
5HT_LYMST	PMLVMMTIYIRLWLV.....ARSRIKDKFQMTKARL...
A1AD_HUMAN	PMAVIVVMYCRVYVV.....A.....RSTTRSL...
A1AD_MOUSE	PMAVIVVMYCRVYVV.....A.....RSTTRSL...
Q13675	PLAILVMYCRVYVV.....A.....KRESRGL...
Q13729	PLAILVMYCRVYVV.....A.....KRESRGL...
O60451	PLAILVMYCRVYVV.....A.....KRESRGL...
A1AA_RAT	PLAILVMYCRVYVV.....A.....KRESRGL...
O54913	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_BOVIN	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_CANFA	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RABIT	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_HUMAN	PLAILVMYCRVYVV.....A.....KRESRGL...
A1AA_ORYLA	PLAILVMYCRVYVV.....A.....OKESRGL...
O96716	PLLIIMLVFYGITFEKA.....A.....RDQARKI...
O75963	PFLVMLVCYGFIERV.....ARV.....KARKV...
HGPRBMY8	PLIIMTIACYSVVECAARRQHA.LLYNVKRHSLEVRVKDCV

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FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	SPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL	EISHVLPTSDEFAKEEEEEEDSESSGQVENGLGNGNDAI.	
5H1A_HUMANTGADTRHGASPAQPK..KSVNG....E..	
5H1A_MOUSEKGAGTSFGTSSAPPPK..KSLNG....Q..	
5H1A_FUGRUKASDMCLTLSPAVFHK..RA.NG....D..	
5HT_LYMSTKTEETTLVASPKTEYSVVSDCNGCNSPD..	
A1AD_HUMANEA.....GVKRER..	
A1AD_MOUSEEA.....GIKREP..	
Q13675KS.....GLKTDK..	
Q13729KS.....GLKTDK..	
O60451KS.....GLKTDK..	
A1AA_RATKS.....GLKTDK..	
O54913KS.....GLKTDK..	
A1AA_BOVINKS.....GLKTDK..	
A1AA_CANFAKS.....GLKTDK..	
A1AA_RABITKS.....GLKTDK..	
A1AA_HUMANKS.....GLKTDK..	
A1AA_ORYLAKE.....GQKIEK..	
O96716NA.....LEG....	
O75963HCGTVVIVEEDAQRTGRKNSSTSTSSSG..	
HGPRBMY8	ENEEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDG	
ACM4_CHICK	QQEEKETSNESSTVSMQTTKDKPTTEILPAGQGQSPAHP	
YDBM_CAEEL	.IEEDECEDEDSDEKRDDHTS...MTTVTATVTGPTA.P	
5H1A_HUMAN	..SGSRNWRLGVESKAGGALCANGAVRQGDDGAAL.EVIE	
5H1A_MOUSE	..PGSGDCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE	
5H1A_FUGRU	..AVSAEWKRGYKFKP..SSPCANGAVRHGEEMESL.EVIE	
5HT_LYMST	..STTEKKKRRAPFKSYG..CSPRPERKKNRAKKL PENAN	
A1AD_HUMAN	..GKAS.....EVVL	
A1AD_MOUSE	..GKAS.....EVVL	
Q13675	..SDSE.....QVTL	
Q13729	..SDSE.....QVTL	
O60451	..SDSE.....QVTL	
A1AA_RAT	..SDSE.....QVTL	
O54913	..SDSE.....QVTL	
A1AA_BOVIN	..SDSE.....QVTL	
A1AA_CANFA	..SDSE.....QVTL	
A1AA_RABIT	..SDSE.....QVTL	
A1AA_HUMAN	..SDSE.....QVTL	
A1AA_ORYLA	..SDSE.....QVIL	
O96716	
O75963	..SRRNAFQGVVYSANQCKALITILVVLGAFMVTWGPYMV	
HGPRBMY8	SLKAKEGSTGTSESSVEARGSEEVRRESSTVASDGSMEGKE	

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FIG. 6F

ACM4_CHICK	R	V	N	P	T	S	K	W	S	K	I	K	I	V	T	K	Q	T	G	T	E	S	V	T	A	I	E	I	V	P	A	K	A	G	A	S	D	H	N	S
YDBM_CAEEL	Y	M	K	R	E	A	K	I	S	K	S	V	P	I	E	K	E	S	A	I	Q	K	R	E	A	K	P	M	R	S	V	M	A	I	S	Y	E	K	V	K
5H1A_HUMAN	.	V	H	R	V	G	N	S	K	E	H	L	P	L	P	S	E	A	G	P	T	.	.	.	P	C	A	P	.	.	.	A	S	F		
5H1A_MOUSE	.	V	H	R	V	G	N	S	K	G	D	L	P	L	P	S	E	S	G	A	T	.	.	.	S	Y	V	P	.	.	.	A	C	L		
5H1A_FUGRU	.	V	N	.	.	S	N	S	K	T	H	L	P	L	.	.	.	P	N	.	.	.	T	.	.	.	P	.	Q	S	.	.	.	S	S	H				
5HT_LYMST	G	V	N	S	N	S	S	S	S	E	R	L	K	Q	I	Q	I	E	T	A	E	A	F	A	N	.	.	.	G	C	A	E	E	A	S	T	A	M	L	
A1AD_HUMAN	R	I	H	C		
A1AD_MOUSE	R	I	H	C			
Q13675	R	I	H	R			
Q13729	R	I	H	R			
O60451	R	I	H	R			
A1AA_RAT	R	I	H	R			
O54913	R	I	H	R			
A1AA_BOVIN	R	I	H	R			
A1AA_CANFA	R	I	H	R			
A1AA_RABIT	R	I	H	R			
A1AA_HUMAN	R	I	H	R			
A1AA_ORYLA	R	M	H	R			
O96716	R	L	E	Q			
O75963	V	I	.	.	.	A	S	E	A	L	W	G	K	S	S	V	S	P	S	L	E	T	W	A	T	.	.	.	W	L	S	F	A	S	A	V	C	H	P	
HGPRBMY8	G	S	T	K	V	E	E	N	S	M	K	A	D	K	G	R	T	E	V	N	Q	C	S	I	D	L	G	E	D	D	M	E	F	G	E	D	D	I	N	F
ACM4_CHICK	L	S	N	S	R	P	A	N	V	A	R	K	F	A	S	T	A	R	S	Q	V	R	K	K	R	O	M	A	A	R	.	.	E	K	K	V	T	R	T	I
YDBM_CAEEL	R	H	K	N	R	K	E	R	I	Y	R	K	.	.	S	T	Q	R	.	.	.	K	P	K	A	I	S	A	A	K	.	.	E	R	R	G	V	K	V	L
5H1A_HUMAN	E	R	K	.	.	N	E	R	N	
5H1A_MOUSE	E	R	K	.	.	N	E	R	T		
5H1A_FUGRU	E	N	I	.	.	N	E	K	T		
5HT_LYMST	E	R	Q	C	N	N	G	K	K	I	S	S	N	D	T	P	Y	S	R	T	R	E	K	L	E	.	.	L	K	R	.	.	E	R	K	A	A	T	L	
A1AD_HUMAN	K	G	.	.	.	H	T	F	R	S	S	L	S	V	
A1AD_MOUSE	K	G	.	.	.	H	T	L	R	S	S	L	S	V		
Q13675	K	T	.	.	.	K	T	.	.	.	H	F	S	V		
Q13729	K	T	.	.	.	K	T	.	.	.	H	F	S	V			
O60451	K	T	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_RAT	K	N	.	.	.	K	T	.	.	.	H	F	S	V			
O54913	K	N	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_BOVIN	K	N	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_CANFA	K	N	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_RABIT	K	N	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_HUMAN	K	T	.	.	.	K	T	.	.	.	H	F	S	V			
A1AA_ORYLA	R	S	.	.	.	R	T	.	.	.	H	F	A	T			
O96716	K			
O75963	L	I	Y	G	L	W	N	K	T	V	R	K	E	L	L	G	M	C	F	G	D	R	Y	Y	R	E	P	F	V	Q	.	.	R	O	R	T	S	R	L	F
HGPRBMY8	S	E	D	D	V	E	A	V	N	I	P	E	S	L	P	P	S	R	R	N	S	N	.	.	N	P	P	L	P	R	C	Y	Q	C	K	A	A	K	V	I

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FIG. 6G

ACM4_CHICK	FALLLAFILTWTPYNMVLINTFC..ETCVPET.VWSIGY
YDBM_CAEEL	GIILGCFTVCWAPFFETMYVLVQFC..KDCSPNAHIEMFIT
5H1A_HUMAN	GIIMGTFILCWLPPFFIVALVLPE.CESSCHMPTLLGAIIN
5H1A_MOUSE	GIIMGTFILCWLPPFFIVALVLPE.CESSCHMPELLGAIIN
5H1A_FUGRU	GIIMGTFILCWLPPFFIVALVLPE.CAENCYMPEWLGAVIN
5HT_LYMST	AIITGAFLICWLPPFFIALIGPF.VDPE.GIPPFARSEFVL
A1AD_HUMAN	AIVVGVFVLCWFPPFFVVLPLGSL.F.POLKPSEGVFKVIF
A1AD_MOUSE	AIVVGVFVLCWFPPFFVVLPLGSL.F.POLKPSEGVFKVIF
Q13675	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPSETVFKIVF
Q13729	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPSETVFKIVF
O60451	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPSETVFKIVF
A1AA_RAT	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPSETVFKIVF
O54913	GIVVGCFVLCWLPPFELVMPIGSF.F.PNFKPPETVFKIVF
A1AA_BOVIN	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFRPPSETVFKIAF
A1AA_CANFA	GIVVGCFVLCWLPPFELVMPIG~~~~~
A1AA_RABIT	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPETVFKIVF
A1AA_HUMAN	GIVVGCFVLCWLPPFELVMPIGSF.F.PDFKPPSETVFKIVF
A1AA_ORYLA	GIVVGCFVLCWLPPFELVLPISG.F.PAYRPSDTVFKITE
O96716	GIIMGVFILCWLPPF.VVNIIVNP.F.CDRCVQPAVFIALT
O75963	SISNRITDLGLSPHLTALMAGGQPLGHSSSTGDTGFSQSQ
HGPRBMY8	FIIFSYVLSLGPYCFIAVT.AVWVDVETQVPQWVITIII
ACM4_CHICK	WLCYVNSTINPACYALCNATFKKTEKHLIMCQYRNIGTAR
YDBM_CAEEL	WLGYSNSAMNPIIYTVFNRDYQIALKRLFTSEKKPSSTSR
5H1A_HUMAN	WLGYSNSLLNPVIYAYFNKDFQNAFKKLIKCKFCRQ~~~~
5H1A_MOUSE	WLGYSNSLLNPVIYAYFNKDFQNAFKKLIKCKFCR~~~~
5H1A_FUGRU	WLGYSNSLLNPVIYAYFNKDFQSAFKKILRCKFHRH~~~~
5HT_LYMST	WLGYNFNSLLNPVIYTFISPEFRSAFQKILFGKYRRGHR~~
A1AD_HUMAN	WLGYNFNSCVNPLIYPCSSREFKRAFLRLLRC.QCRRRRR.
A1AD_MOUSE	WLGYNFNSCVNPLIYPCSSREFKRAFLRLLRC.QCRRRRR.
Q13675	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
Q13729	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
O60451	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
A1AA_RAT	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
O54913	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
A1AA_BOVIN	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
A1AA_CANFA	~~~~~
A1AA_RABIT	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
A1AA_HUMAN	WLGYNLNSCINPIIYPCSSQEFKKAFQNVLR.QCLRKRKQS
A1AA_ORYLA	WLGYNLNSCINPIIYPCSNQEFKKAFQSLGV.HCLRMTPR
O96716	WLGWINSCFNPIIY.AFNKEFRKVFVKMICCHKCRGVTVG
O75963	DSGNLRAL~~~~~
HGPRBMY8	WLFELQCCIHPIYVYGYMHKTIKKEIQDMLKKKFFCKEKPPK

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FIG. 6H

```

ACM4_CHICK ~~~~~
YDBM_CAEEL V~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN .RRPLWRVY..GHHWRASTSGLRQDCAPSSGDAPPGAPLA
A1AD_MOUSE .R..LW.....PSLRPPLAST...DRRPA LR LCPQPAHRT
Q13675 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
Q13729 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
O60451 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_RAT SKH...ALG..YT.LHPPSQAVEGQHRDM.VRIPVGSGET
O54913 SKH...ALG..YT.LHPPSQAVEEQHRGM.VRIPVGSGET
A1AA_BOVIN SKH...TLG..YT.LHAPSHVLEGGQHKDL.VRIPVGS AET
A1AA_CANFA ~~~~~
A1AA_RABIT SKH...ALG..YT.LHAPSQALEGGQHKDM.VRIPVGSGET
A1AA_HUMAN SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_ORYLA AH H H H L S V G . . Q S Q T Q G H S L T I S L D S K G A P C R L S P S S S V A
O96716 P N H A D L N Y D P V A M R L K K R G E N A N G T V N G D A N G K A N G N I E A
O75963 ~~~~~
HGPRBMY8 E D S H P D L P G T E G G T E G K I V P S Y D S A T F P ~~~~~

ACM4_CHICK ~~~~~
YDBM_CAEEL ~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN LTALPDPD..PEP...PGTPEMQAPVASRRKPPSA...FR
A1AD_MOUSE PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASLRLR
Q13675 FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTART
Q13729 FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARG
O60451 FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARR
A1AA_RAT FYKISKTDGVCEWKFFSSMPQGSARITV PKDQSACTTARV
O54913 FYKISKTDGVCEWKFFSSMPQGSARITMPKDQSACTTARV
A1AA_BOVIN FYKISKTDGVCEWKIFSSSLPRGSARM A V A R D P S A C T T A R V
A1AA_CANFA ~~~~~
A1AA_RABIT FYKISKTDGVCEWKFFSSMPRGSARITV PKDQSACTTARV
A1AA_HUMAN FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARV
A1AA_ORYLA L S R T P S S R D S R E W R V F S G G P I N S G . . P G P T E A G R A K V A K L
O96716 G E G T S S S ~~~~~
O75963 ~~~~~
HGPRBMY8 ~~~~~

```

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FIG. 6I

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAAACQ
A1AD_MOUSE	EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675	KRSRVTRLECS...GMILAHCN..LRLPGSRDSPASASQ
Q13729	HT.PMT~~~~~
O60451	GMDCRYFTKNC...REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT	RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913	RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN	RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA	~~~~~
A1AA_RABIT	RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN	RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA	CNKSLHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSE
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE	RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675	AAGTTGDVPPGRRHQALIFVFLVETGFHHVGQDDLDDLLT
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	NGEEV~~~~~
O54913	NGEEV~~~~~
A1AA_BOVIN	NGEEV~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	NGEEV~~~~~
A1AA_HUMAN	NGEEV~~~~~
A1AA_ORYLA	KGESV~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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FIG. 6J

ACM4_CHICK	~
YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPRBMY8	~

FIG. 7

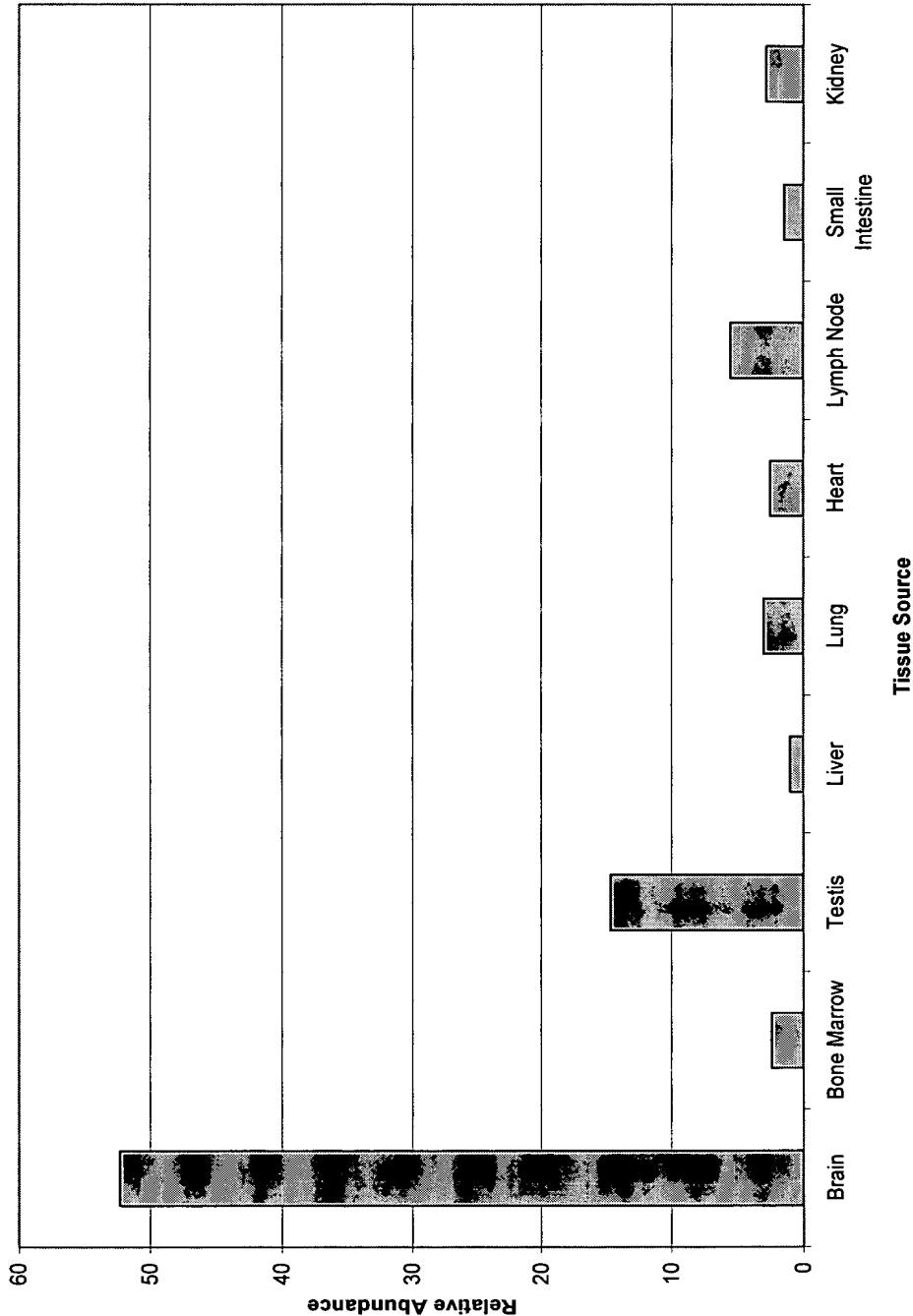
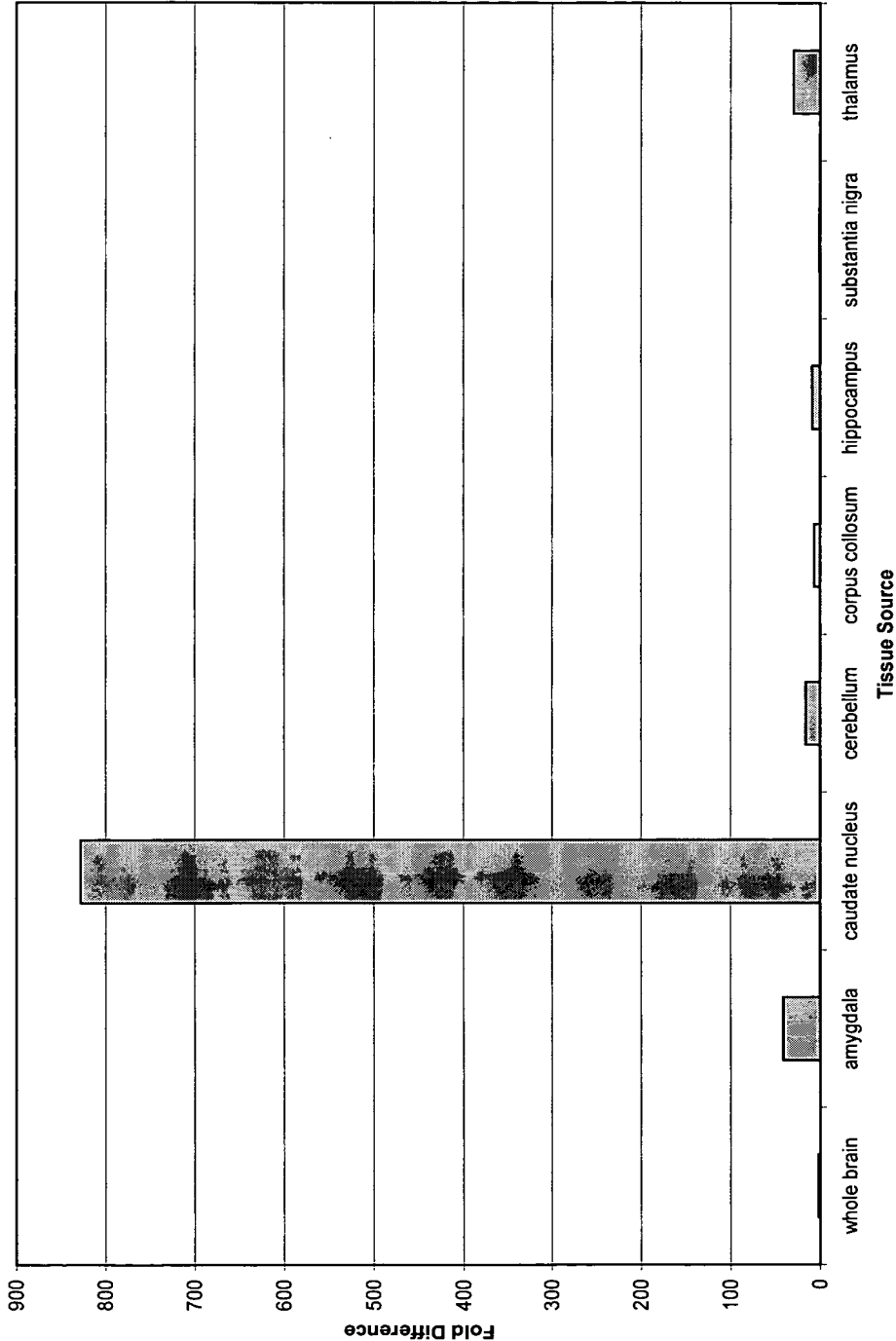


FIG. 8



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FIG. 9

HGPRBM8	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AL390879	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX148250	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX080495	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
HGPRBM8	QLLQVTNRFIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AL390879	QLLQVTNRFIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX148250	QLLQVTNRFIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX080495	QLLQVTNRFIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
HGPRBM8	TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AL390879	TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX148250	TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX080495	TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
HGPRBM8	LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AL390879	LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX148250	LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX080495	LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
HGPRBM8	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AL390879	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX148250	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX080495	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
HGPRBM8	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AL390879	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX148250	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX080495	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
HGPRBM8	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AL390879	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AX148250	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AX080495	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
HGPRBM8	LAVWVDVETQVPQWVITIIIWLFFLQCCIHYPYVGYMHKTIKKEIQDMLKKFFCCKEPPK
AL390879	LAVWVDVETQVPQWVITIIIWLFFLQCCIHYPYVGYMHKTIKKEIQDMLKKFFCCKEPPK
AX148250	LAVWVDVETQVPQWVITIIIWLFFLQCCIHYPYVGYMHKTIKKEIQDMLKKFFCCKEPPK
AX080495	LAVWVDVETQVPQWVITIIIWLFFLQCCIHYPYVGYMHKTIKKEIQDMLKKFFCCKEPPK
HGPRBM8	EDSHPDLPGTEGGTEGKIVPSYDSATFP~
AL390879	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX148250	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX080495	EDSHPDLPGTEGGTEGKIVPSYDSATFP*

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FIG. 10A

AX080495 GCCTGCAACCTGTCYCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
HGPRBMY8 ~~~~GCAACCTGTCCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
AL390879 ~~~~~~ATGACGTCCACCTGC
AX148250 ~~~~~~ATGACGTCCACCTGC

AX080495 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
HGPRBMY8 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AL390879 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AX148250 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC

AX080495 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
AL390879 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
AX148250 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
HGPRBMY8 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AL390879 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AX148250 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG

AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
HGPRBMY8 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AL390879 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AX148250 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
HGPRBMY8 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AL390879 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX148250 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC

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FIG. 10B

AX080495	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBMY8	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX080495	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBMY8	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX080495	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBMY8	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX080495	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
HGPRBMY8	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AL390879	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX148250	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX080495	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
HGPRBMY8	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AL390879	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AX148250	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AX080495	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBMY8	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX080495	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBMY8	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX080495	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBMY8	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX080495	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBMY8	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX080495	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBMY8	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA

FIG. 10C

AX080495	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX080495	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATG[CATGGAGTTT
HGPRBMY8	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX080495	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AL390879	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX148250	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX080495	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
HGPRBMY8	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AL390879	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AX148250	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AX080495	TGCCCAGGTGCTACCAAGTGCTAAAGCTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8	TGCCCAGGTGCTACCAAGTGCTAAAGCTGCTAAAGTGATCTTCATCATCATT
AL390879	TGCCCAGGTGCTACCAAGTGCTAAAGCTGCTAAAGTGATCTTCATCATCATT
AX148250	TGCCCAGGTGCTACCAAGTGCTAAAGCTGCTAAAGTGATCTTCATCATCATT
AX080495	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
HGPRBMY8	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AL390879	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AX148250	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AX080495	CGTGTGGGTGGATGTGCAAAACCAGGTACCCAGTGGGTGATCACCATAA
HGPRBMY8	CGTGTGGGTGGATGTGCAAAACCAGGTACCCAGTGGGTGATCACCATAA
AL390879	CGTGTGGGTGGATGTGCAAAACCAGGTACCCAGTGGGTGATCACCATAA
AX148250	CGTGTGGGTGGATGTGCAAAACCAGGTACCCAGTGGGTGATCACCATAA
AX080495	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX080495	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX080495	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
HGPRBMY8	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AL390879	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AX148250	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG

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FIG. 10D

```
AX080495 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
HGPRBMY8 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AL390879 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AX148250 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT

AX080495 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAATCAGTCCTTCA
HGPRBMY8 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~
AL390879 ACTTTTCCTTGA~~~~~
AX148250 ACTTTTCCTTGA~~~~~

AX080495 GCCACAGCTATTTAGAGCTTTAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8 ~~~~~
AL390879 ~~~~~
AX148250 ~~~~~

AX080495 CTTTCTGTG
HGPRBMY8 ~~~~~
AL390879 ~~~~~
AX148250 ~~~~~
```

FIG. 11

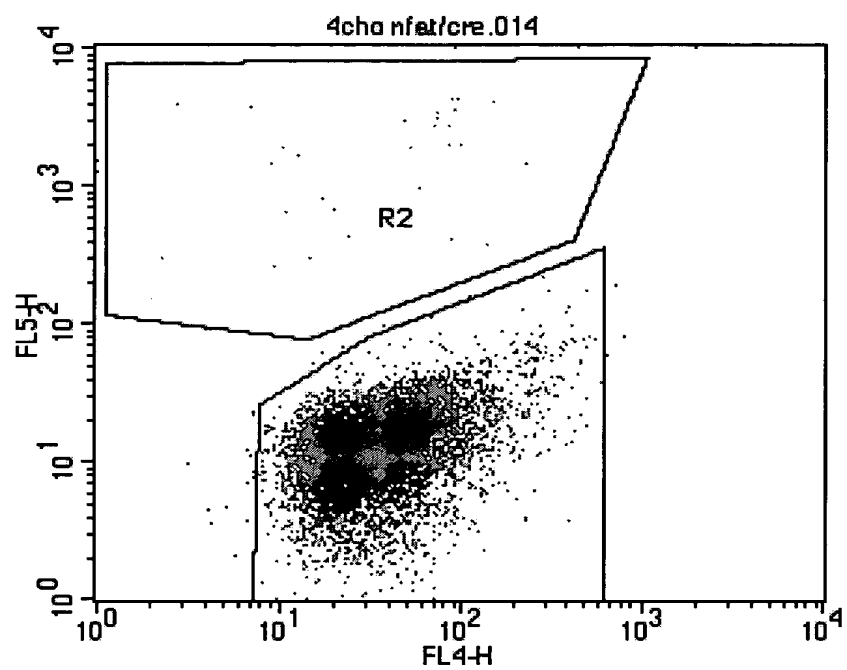
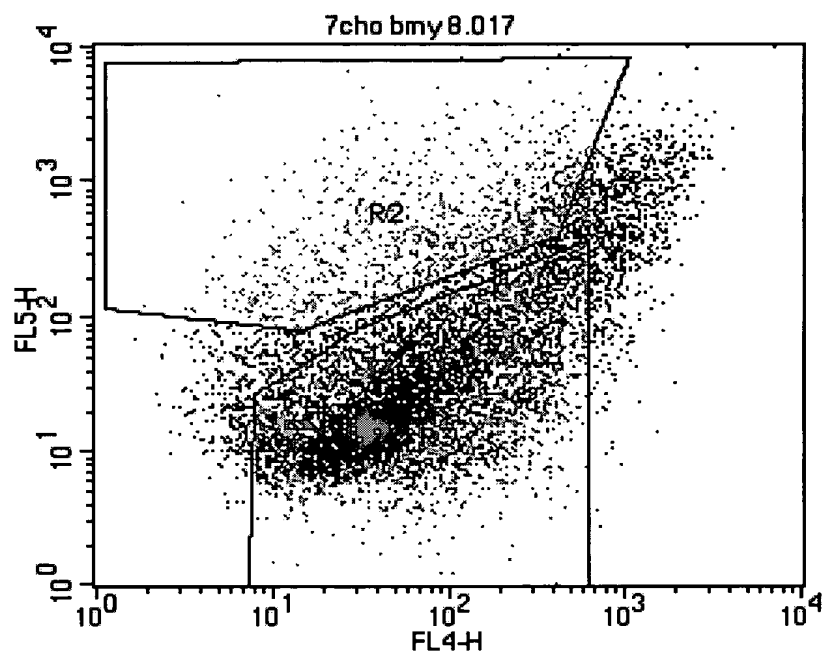


FIG. 12



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FIG. 13

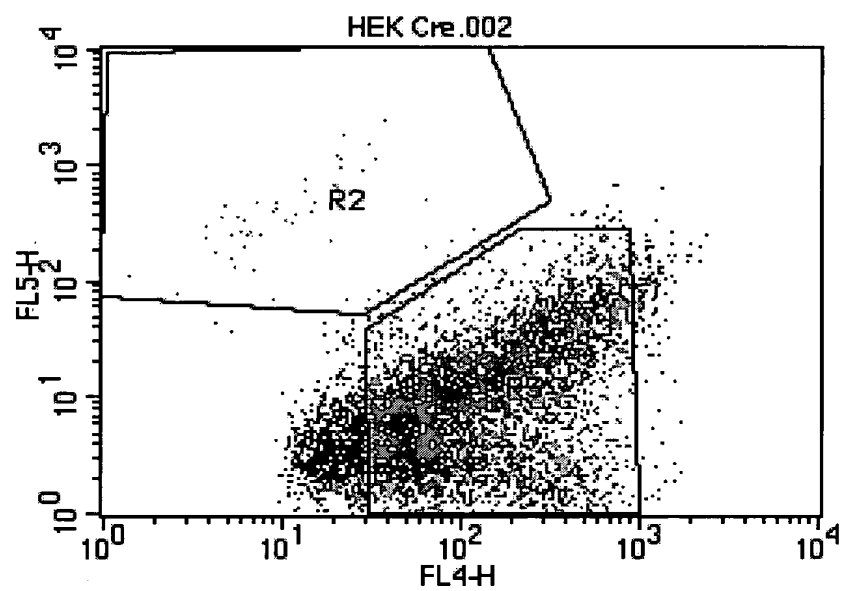


FIG. 14

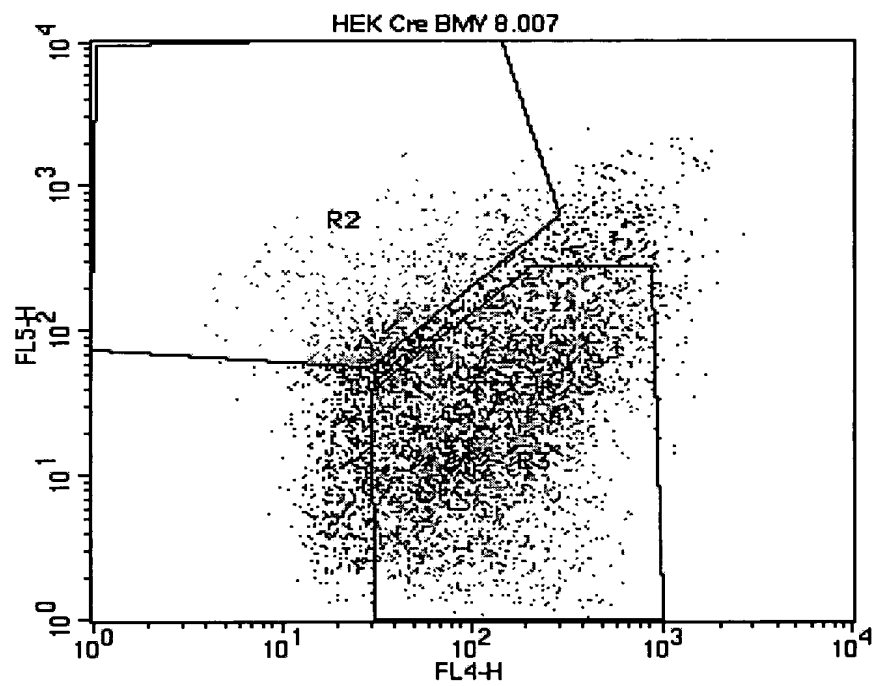
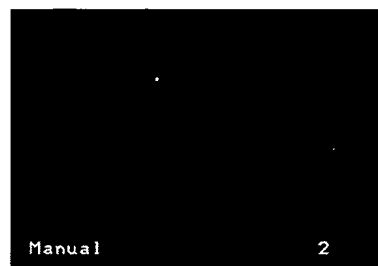
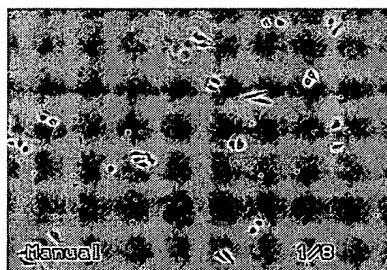


FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)

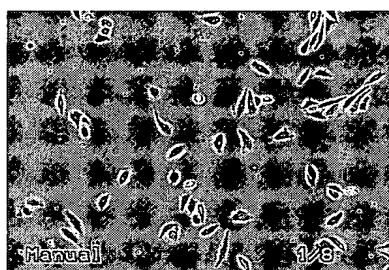
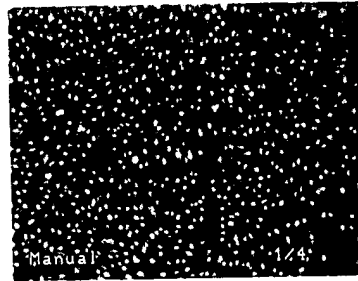
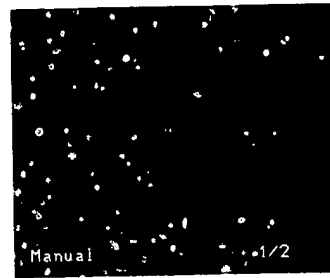


FIG. 16

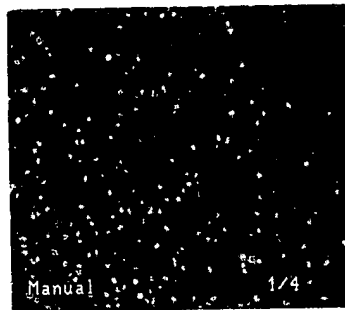
a. CHO-NFAT CRE



b. CHO-NFAT/CRE + FT/P



c. CHO-NFAT CRE oGPCR-Intermediate



d. CHO-NFAT/CRE oGPCR high

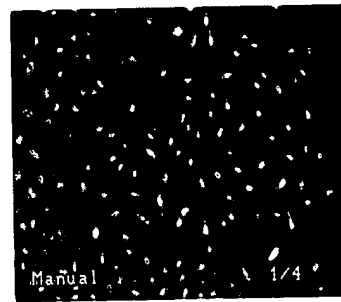
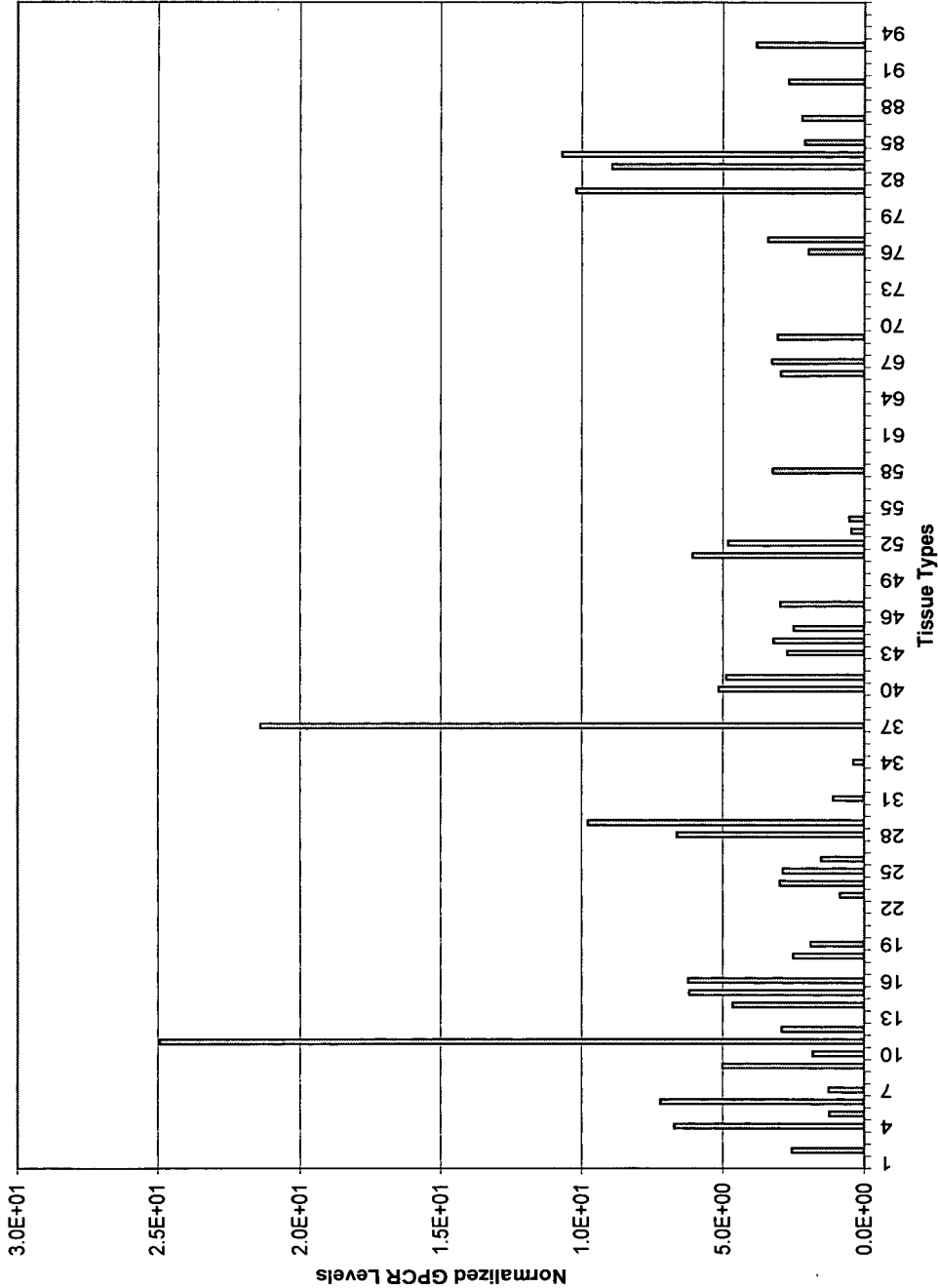


FIG. 17



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FIG. 18A

1	ATGACGTCCACCTGCACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC	60
1	M T S T C T N S T R E S N S S H T C M P	20
61	CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC	120
21	L S K M P I S L A H G I I R S T V L V I	40
121	TTCCTCGCCGCCTCTTTTCGTGGCAACATAGTGCTGGCGCTAGTGTTCAGCGCAAGCCG	180
41	F L A A S F V G N I V L A L V L Q R K P	60
181	CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG	240
61	Q L L Q V T N R F I F N L L V T D L L Q	80
241	ATTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTCTGGCCCCCTCAAC	300
81	I S L V A P W V V A T S V P L F W P L N	100
301	AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTGCGCTTCGCCAGCGTCAAC	360
101	S H F C T A L V S L T H L F A F A S V N	120
361	ACCATTGTCNTGGTGTCACTGGATCGCTACTTGTCCATCATCCACCCTCTCTCTACCCG	420
121	T I V <u>X</u> V S V D R Y L S I I H P L S Y P	140
421	TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCTCTATGGCACCTGGATTGTGGCCATC	480
141	S K M T Q R R G Y L L L Y G T W I V A I	160
481	CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT	540
161	L Q S T P P L Y G W G Q A A F D E R N A	180
541	CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTTC	600
181	L C S M I W G A S P S Y T I L S V V S F	200
601	ATCGTCATTCCACTGATTGTATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGG	660
201	I V I P L I V M I A C Y S V V F C A A R	220
661	AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC	720
221	R Q H A L L Y N V K R H S L E V R V K D	240
721	TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTCCAGGATGAGAGT	780
241	C V E N E D E E G A E K K E E F Q D E S	260
781	GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG	840
261	E F R R Q H E G E V K A K E G R M E A K	280
841	GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAAGTGAGAGTAGTGTAGAGGCC	900
281	D G S L K A K E G S T G T S E S S V E A	300

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FIG. 18B

901	AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT	960
301	R G S E E V R E S S T V A S D G S M E G	320
961	AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG	1020
321	K E G S T K V E E N S M K A D K G R T E	340
1021	GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC	1080
341	V N Q C S I D L G E D <u>X</u> M E F G E D D I	360
1081	AATTTCACTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCACCCAGTCGT	1140
361	N F S E D D V E A V N I P E S L P P S R	380
1141	CGTAACAGCAACAGCAACCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTNNNAAGTG	1200
381	R N S N S N P P L P R C Y Q C K A <u>X</u> K V	400
1201	ATCTTCATCATATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTCAGCAGTC	1260
401	I F I I I F S Y V L S L G P Y C F L A V	420
1261	CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC	1320
421	L A V W V D V E T Q V P Q W V I T I I I	440
1321	TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC	1380
441	W L F F L Q C C I H P Y V Y G Y M H K T	460
1381	ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA	1440
461	I K K E I Q D M L K K F F C K E K P P K	480
1441	GAAGATAGCCACCCAGACCTGCCCCGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT	1500
481	E D S H P D L P G T E G G T E G K I V P	500
1501	TCCTACGATTCTGCTACTTTTCCTTGA	1527
501	S Y D S A T F P	508

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FIG. 19

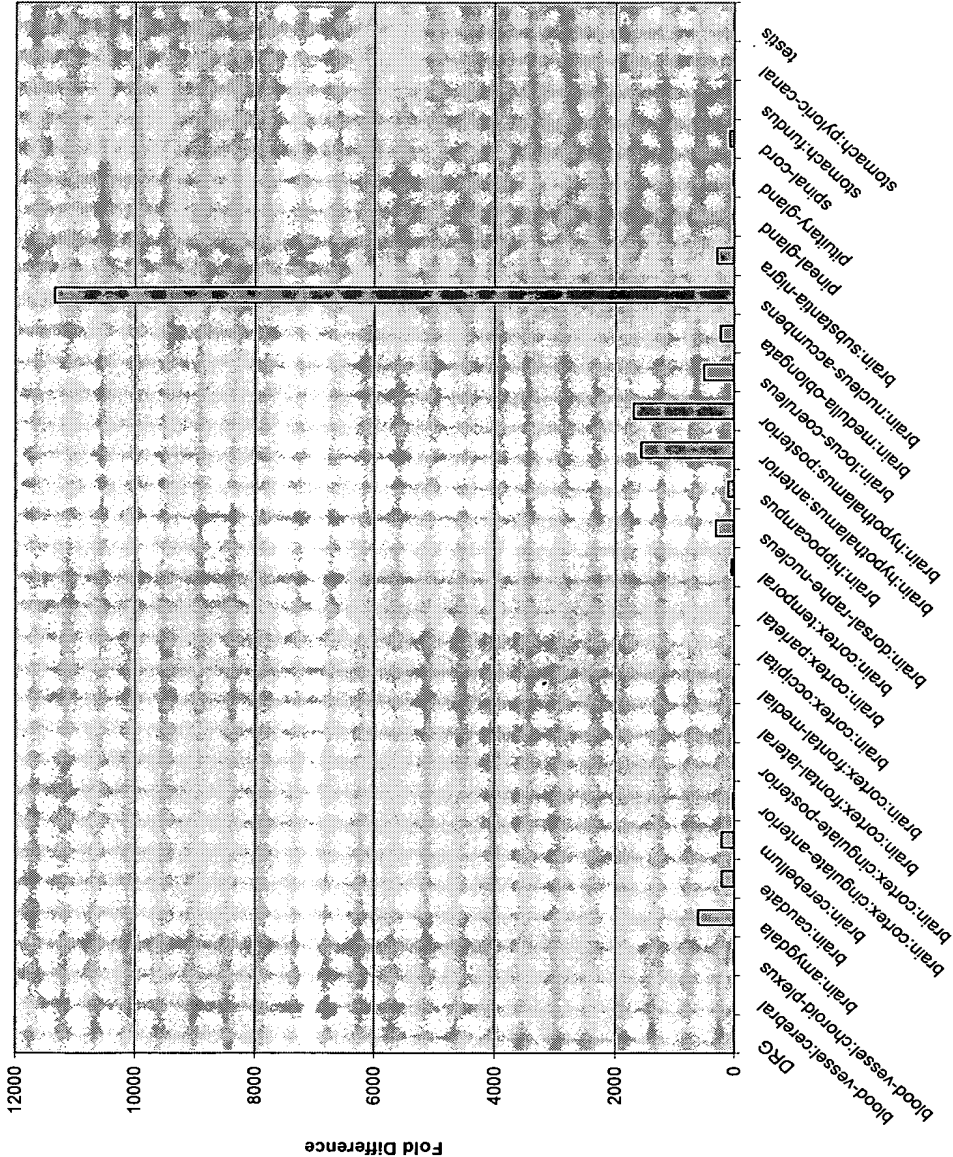


FIG. 20

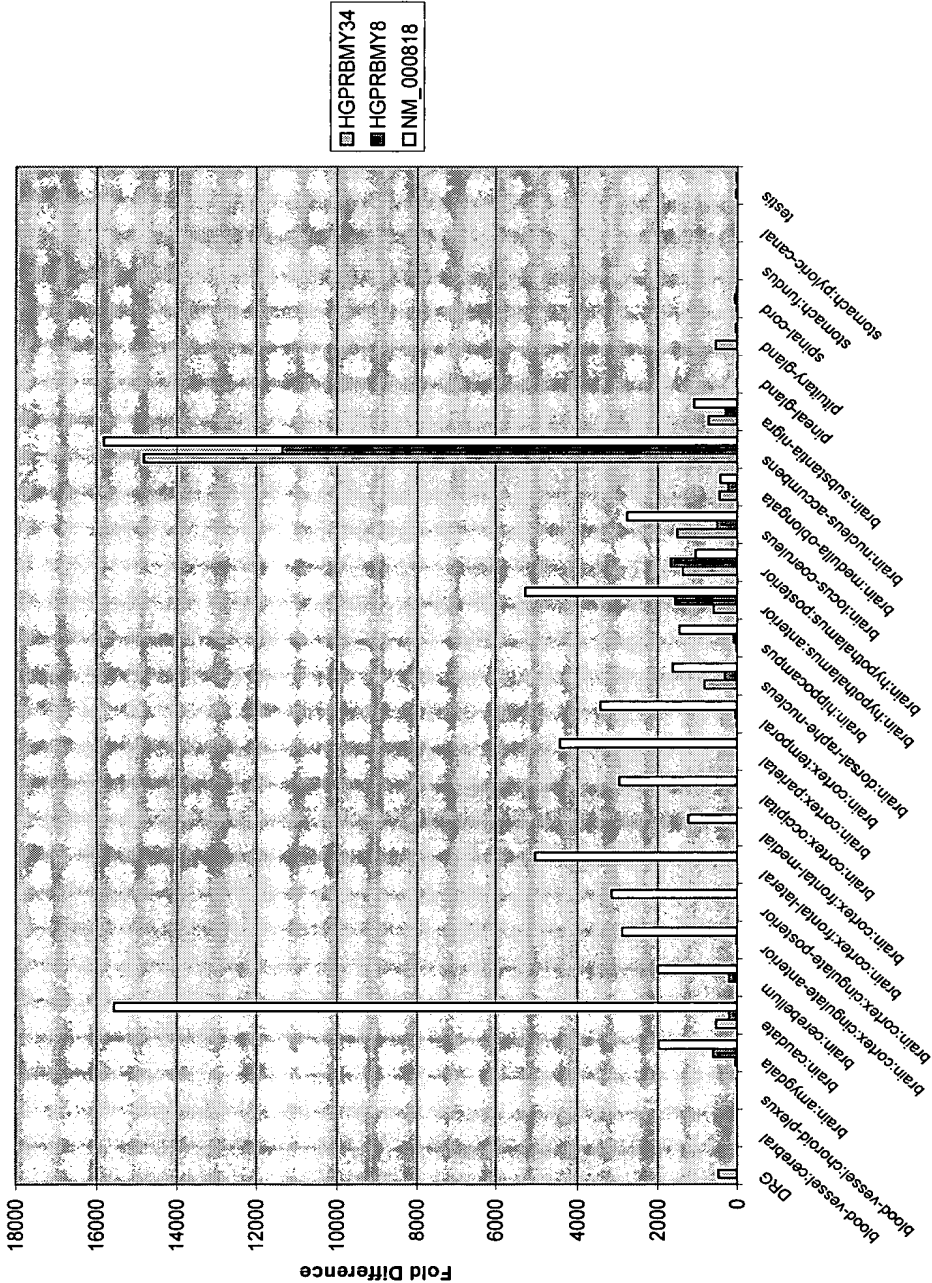


FIG. 21

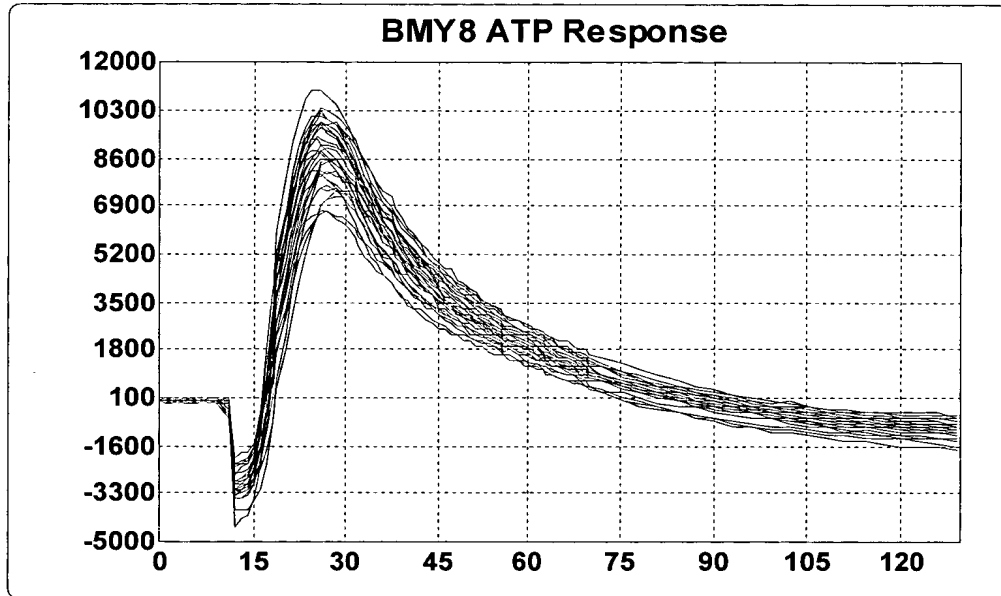


FIG. 22

